Amendments to the Specification:

Please replace the paragraph beginning on page 1, line 8 with the following amended paragraph:

--This application is a divisional of U.S. Patent Application Serial No. 09/881,239, filed June 14, 2001, which is related to provisional patent application serial nos. 60/212,082, filed June 15, 2000; 60/280,867, filed April 2, 2001; and 60/280,811, filed April 2, 2001, from which applications priority is claimed under 35 USC § §§ 120 and 119(e)(1) and which applications are incorporated herein by reference in their entireties.--

Please replace the paragraph beginning on page 9, line 22 with the following rewritten paragraph:

-- Figure 3 (SEQ ID NO:1) depicts the amino acid sequence of a representative NS3/4a conformational antigen for use in the present assays. The bolded alanine at position 182 is substituted for the native serine normally present at this position.--

Please replace the paragraph beginning on page 9, line 25 with the following rewritten paragraph:

-- Figures 4A through 4D depict the DNA (SEQ ID NO:2) and corresponding amino acid (SEQ ID NO:3) sequence of another representative NS3/4a conformational antigen for use in the present assays. The amino acids at positions 403 and 404 of Figures 4A through 4D represent substitutions of Pro for Thr, and Ile for Ser, of the native amino acid sequence of HCV-1.--

Please replace the paragraph beginning on page 10, line 1 with the following rewritten paragraph:

-- Figures 7A-7F depict the DNA (SEQ ID NO:4) and corresponding amino acid (SEQ ID NO:5) sequence of MEFA 12.--

Please replace the paragraph beginning on page 27, line 5 with the following rewritten paragraph:

-- For example, epitopes derived from, e.g., the hypervariable region of E2, such as a region spanning amino acids 384-410 or 390-410, can be included in the MEFA antigen. A particularly effective E2 epitope is one which includes a consensus sequence derived from this region, such as the consensus sequence Gly-Ser-Ala-Ala-Arg-Thr-Thr-Ser-Gly-Phe-Val-Ser-Leu-Phe-Ala-Pro-Gly-Ala-Lys-Gln-Asn (SEQ ID NO:6), which represents a consensus sequence for amino acids 390-410 of the HCV type 1 genome. A representative E2 epitope present in a MEFA of the invention can comprise a hybrid epitope spanning amino acids 390-444. Such a hybrid E2 epitope can include a consensus sequence representing amino acids 390-410 fused to the native amino acid sequence for amino acids 411-444 of HCV E2.--

Please replace the paragraph beginning on page 51, line 30 with the following rewritten paragraph:

-- Next, the following fragments were ligated together: (a) a 761 bp *Hind*III-*Cla*I fragment from pSP721aHC #1 (pSP72.1aHC was generated by ligating together the following: pSP72 which had been digested with *Hind*III and *Cla*I, synthetic oligonucleotides which would provide a 5' *Hind*III cloning site, followed by the sequence ACAAAACAAA (SEQ ID NO:7), the initiation codon ATG, and codons for HCV1a, beginning with amino acid 1027 and continuing to a *Bgl*II site at amino acid 1046, and a 683 bp *Bgl*II-*Cla*I restriction fragment (encoding amino acids 1046-1274) from pAcHLTns3ns4aPI); (b) a 1353 bp *Bam*HI-*Hind*III fragment for the yeast hybrid promoter ADH2/GAPDH; (c) a 1320 bp *Cla*I-*Sal*I fragment (encoding HCV1a amino acids 1046-1711 with Thr 1428 mutated to Pro and Ser 1429 mutated to Ile) from pAcHLTns3ns4aPI; and (d) the pBS24.1 yeast expression vector which had been digested with *Bam*HI and *Sal*I, dephosphorylated and gel-purified. The ligation mixture was transformed into competent HB101 and plated on Luria agar plates containing 100 μg/ml ampicillin. Miniprep analyses of individual colonies led to the identification of clones with the expected 3446 bp *Bam*HI-*Sal*I insert which was comprised of the ADH2/GAPDH promoter, the initiator codon ATG and HCV1a NS3/4a from amino acids 1027-1711 (shown as amino acids 1-686 of Figures 4A-4D), with Thr 1428 (amino acid position 403 of Figures 4A-4D) mutated to

Pro and Ser 1429 (amino acid position 404 of Figures 4A-4D) mutated to Ile. The construct was named pd.HCV1a.ns3ns4aPI (see, Figure 5).--

Please replace the paragraph beginning on page 54, line 12 with the following rewritten paragraph:

Additionally, protease enzyme activity was monitored during purification as follows. An NS4A peptide (KKGSVVIVGRIVLSGKPAIIPKK (SEQ ID NO:8)), and the sample containing the NS3/4a conformational epitope, were diluted in 90 µl of reaction buffer (25 mM Tris, pH 7.5, 0.15M NaCl, 0.5 mM EDTA, 10% glycerol, 0.05 n-Dodecyl B-D-Maltoside, 5 mM DTT) and allowed to mix for 30 minutes at room temperature. 90 µl of the mixture were added to a microtiter plate (Costar, Inc., Corning, NY) and 10 µl of HCV substrate (AnaSpec, Inc., San Jose CA) was added. The plate was mixed and read on a Fluostar plate reader. Results were expressed as relative fluorescence units (RFU) per minute.